



# SEQUENCE LISTING

<110> Pavlakis, George N.  
The Government of the United States of America  
as represented by The Secretary of the  
Department of Health and Human Services

<120> Molecular Clones With Mutated HIV gag/pol, SIV gag and  
SIV env Genes

<130> 015280-257300US

<140> US 10/644,027  
<141> 2003-08-19

<150> US 60/173,036  
<151> 1999-12-23

<150> WO PCT/US00/34985  
<151> 2000-12-22

<150> US 09/872,733  
<151> 2001-06-01

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<170> PatentIn Ver. 2.1

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<223> Description of Artificial Sequence:wild-type pol region in plasmid pCMVgagpolBNkan

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:mutated pol  
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:mutated

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<210> 5

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus

sequence of mutated SIVgagDX and wild type

Simian (macaque) immunodeficiency virus

isolate 239, clone lambda siv 239-1 in Fig. 4

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<210> 6

<211> 8366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:packaging  
construct pCMVgagpolBNkan

<400> 6

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<210> 7

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:translation of  
complementary strand positions 7814-7002 of  
packaging construct pCMVgagpolBNkan (SEQ ID NO:6)

<400> 7

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Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp
          35          40          45
Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp
          50          55          60
Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro
          65          70          75          80
Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu
          85          90          95
Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu
          100          105          110
Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu
          115          120          125
Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp
          130          135          140
Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu
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Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu
          165          170          175
Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser
          180          185          190

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				245					250					255	
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<210> 8

<211> 8937

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:transfer  
construct 1, pmBCwCNluci

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 mutated SIV env gene

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CMVkan/R-R-SIVenvCTE, mutated SIV env

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Thr Thr Ala Ser Thr Thr Ser Thr Thr Ala Ser Ala Lys Val Asp Met  
130 135 140  
Val Asn Glu Thr Ser Ser Cys Ile Ala Gln Asp Asn Cys Thr Gly Leu  
145 150 155 160  
Glu Gln Glu Gln Met Ile Ser Cys Lys Phe Asn Met Thr Gly Leu Lys  
165 170 175  
Arg Asp Lys Lys Lys Glu Tyr Asn Glu Thr Trp Tyr Ser Ala Asp Leu  
180 185 190  
Val Cys Glu Gln Gly Asn Asn Thr Gly Asn Glu Ser Arg Cys Tyr Met  
195 200 205  
Asn His Cys Asn Thr Ser Val Ile Gln Glu Ser Cys Asp Lys His Tyr  
210 215 220  
Trp Asp Ala Ile Arg Phe Arg Tyr Cys Ala Pro Pro Gly Tyr Ala Leu  
225 230 235 240  
Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Met Pro Lys Cys Ser  
245 250 255  
Lys Val Val Val Ser Ser Cys Thr Arg Met Met Glu Thr Gln Thr Ser  
260 265 270  
Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile  
275 280 285  
Tyr Trp His Gly Arg Asp Asn Arg Thr Ile Ile Ser Leu Asn Lys Tyr  
290 295 300  
Tyr Asn Leu Thr Met Lys Cys Arg Arg Pro Gly Asn Lys Thr Val Leu  
305 310 315 320  
Pro Val Thr Ile Met Ser Gly Leu Val Phe His Ser Gln Pro Ile Asn  
325 330 335  
Asp Arg Pro Lys Gln Ala Trp Cys Trp Phe Gly Gly Lys Trp Lys Asp  
340 345 350  
Ala Ile Lys Glu Val Lys Gln Thr Ile Val Lys His Pro Arg Tyr Thr  
355 360 365

Gly	Thr	Asn	Asn	Thr	Asp	Lys	Ile	Asn	Leu	Thr	Ala	Pro	Gly	Gly	Gly		
	370					375					380						
Asp	Pro	Glu	Val	Thr	Phe	Met	Trp	Thr	Asn	Cys	Arg	Gly	Glu	Phe	Leu		
385					390					395					400		
Tyr	Cys	Lys	Met	Asn	Trp	Phe	Leu	Asn	Trp	Val	Glu	Asp	Arg	Asn	Thr		
				405					410					415			
Ala	Asn	Gln	Lys	Pro	Lys	Glu	Gln	His	Lys	Arg	Asn	Tyr	Val	Pro	Cys		
			420					425					430				
His	Ile	Arg	Gln	Ile	Ile	Asn	Thr	Trp	His	Lys	Val	Gly	Lys	Asn	Val		
	435						440					445					
Tyr	Leu	Pro	Pro	Arg	Glu	Gly	Asp	Leu	Thr	Cys	Asn	Ser	Thr	Val	Thr		
	450					455					460						
Ser	Leu	Ile	Ala	Asn	Ile	Asp	Trp	Ile	Asp	Gly	Asn	Gln	Thr	Asn	Ile		
465					470					475					480		
Thr	Met	Ser	Ala	Glu	Val	Ala	Glu	Leu	Tyr	Arg	Leu	Glu	Leu	Gly	Asp		
				485					490					495			
Tyr	Lys	Leu	Val	Glu	Ile	Thr	Pro	Ile	Gly	Leu	Ala	Pro	Thr	Asp	Val		
			500				505						510				
Lys	Arg	Tyr	Thr	Thr	Gly	Gly	Thr	Ser	Arg	Asn	Lys	Arg	Gly	Val	Phe		
	515						520					525					
Val	Leu	Gly	Phe	Leu	Gly	Phe	Leu	Ala	Thr	Ala	Gly	Ser	Ala	Met	Gly		
	530					535					540						
Ala	Ala	Ser	Leu	Thr	Leu	Thr	Ala	Gln	Ser	Arg	Thr	Leu	Leu	Ala	Gly		
545					550					555					560		
Ile	Val	Gln	Gln	Gln	Gln	Gln	Leu	Leu	Asp	Val	Val	Lys	Arg	Gln	Gln		
				565					570					575			
Glu	Leu	Leu	Arg	Leu	Thr	Val	Trp	Gly	Thr	Lys	Asn	Leu	Gln	Thr	Arg		
			580					585					590				
Val	Thr	Ala	Ile	Glu	Lys	Tyr	Leu	Lys	Asp	Gln	Ala	Gln	Leu	Asn	Ala		
	595						600					605					
Trp	Gly	Cys	Ala	Phe	Arg	Gln	Val	Cys	His	Thr	Thr	Val	Pro	Trp	Pro		
	610					615					620						
Asn	Ala	Ser	Leu	Thr	Pro	Lys	Trp	Asn	Asn	Glu	Thr	Trp	Gln	Glu	Trp		
625					630					635					640		
Glu	Arg	Lys	Val	Asp	Phe	Leu	Glu	Glu	Asn	Ile	Thr	Ala	Leu	Leu	Glu		
				645					650					655			
Glu	Ala	Gln	Ile	Gln	Gln	Glu	Lys	Asn	Met	Tyr	Glu	Leu	Gln	Lys	Leu		
			660					665					670				
Asn	Ser	Trp	Asp	Val	Phe	Gly	Asn	Trp	Phe	Asp	Leu	Ala	Ser	Trp	Ile		
		675					680					685					
Lys	Tyr	Ile	Gln	Tyr	Gly	Val	Tyr	Ile	Val	Val	Gly	Val	Ile	Leu	Leu		
	690					695					700						
Arg	Ile	Val	Ile	Tyr	Ile	Val	Gln	Met	Leu	Ala	Lys	Leu	Arg	Gln	Gly		
705					710					715					720		
Tyr	Arg	Pro	Val	Phe	Ser	Ser	Pro	Pro	Ser	Tyr	Phe	Gln	Gln	Thr	His		
				725					730					735			
Ile	Gln	Gln	Asp	Pro	Ala	Leu	Pro	Thr	Arg	Glu	Gly	Lys	Glu	Arg	Asp		
			740					745					750				
Gly	Gly	Glu	Gly	Gly	Gly	Asn	Ser	Ser	Trp	Pro	Trp	Gln	Ile	Glu	Tyr		
		755					760					765					
Ile	His	Phe	Leu	Ile	Arg	Gln	Leu	Ile	Arg	Leu	Leu	Thr	Trp	Leu	Phe		
	770					775					780						
Ser	Asn	Cys	Arg	Thr	Leu	Leu	Ser	Arg	Val	Tyr	Gln	Ile	Leu	Gln	Pro		
785					790					795					800		
Ile	Leu	Gln	Arg	Leu	Ser	Ala	Thr	Leu	Gln	Arg	Ile	Arg	Glu	Val	Leu		
				805					810					815			
Arg	Thr	Glu	Leu	Thr	Tyr	Leu	Gln	Tyr	Gly	Trp	Ser	Tyr	Phe	His	Glu		
			820					825					830				
Ala	Val	Gln	Ala	Val	Trp	Arg	Ser	Ala	Thr	Glu	Thr	Leu	Ala	Gly	Ala		
		835					840					845					

Trp Gly Asp Leu Trp Glu Thr Leu Arg Arg Gly Gly Arg Trp Ile Leu  
850 855 860  
Ala Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Leu Thr Leu Leu  
865 870 875

<210> 17  
<211> 271  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:translation of  
complementary strand positions 6426-5611 of  
vector CMVkan/R-R-SIVenvCTE (SEQ ID NO:15)

<400> 17  
Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn  
1 5 10 15  
Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn  
20 25 30  
Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp  
35 40 45  
Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp  
50 55 60  
Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro  
65 70 75 80  
Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu  
85 90 95  
Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu  
100 105 110  
Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu  
115 120 125  
Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp  
130 135 140  
Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu  
145 150 155 160  
Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu  
165 170 175  
Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser  
180 185 190  
Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu  
195 200 205  
Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp  
210 215 220  
Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser  
225 230 235 240  
Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro  
245 250 255  
Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe  
260 265 270

<210> 18  
<211> 2640  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: coding sequence of  
mutated lentiviral env from "env-coding" vector  
CMVkan/R-R-SIVenvCTE, coding sequence of  
mutated SIV env in vector CMVkan/R-R-SIVgpl60CTE

<400> 18

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tattgtactc tatatgtcac agtcttttat ggtgtaccag cttggaggaa tgcgacaatt 120
cccctctttt gtgcaaccaa gaatagggat acttggggaa caactcagtg cctaccagat 180
aatggtgatt attcagaagt ggcccttaat gttacagaaa gctttgatgc ctggaataat 240
acagtcacag aacaggcaat agaggatgta tggcaactct ttgagacctc aataaagcct 300
tgtgtaaaat tatccccatt atgcattact atgagatgca ataaaagtga gacagataga 360
tggggattga caaaatcaat aacaacaaca gcatcaaca catcaacgac agcatcagca 420
aaagtagaca tgggtcaatga gactagtctt tgtatagccc aggataattg cacaggcttg 480
gaacaagagc aaatgataag ctgtaaattc aacatgacag ggtaaaaaag agacaagaaa 540
aaagagtaca atgaaacttg gtactctgca gatttggtat gtgaacaagg gaataacact 600
ggtaatgaaa gtagatgtta catgaaccac tgtaacactt ctgttatcca agagtcttgt 660
gacaaacatt attgggatgc tattagattt aggtattgtg cacctccagg ttatgctttg 720
cttagatgta atgacacaaa ttattcaggc tttatgccta aatgttctaa ggtggtggtc 780
tcttcatgca caaggatgat ggagacacag acttctactt ggtttggtt taatggaact 840
agagcagaaa atagaactta tatttactgg catggtaggg ataataggac tataattagt 900
ttaaataagt attataatct aacaatgaaa tgtagaagac caggaaataa gacagtttta 960
ccagtcacca ttatgtctgg attggttttc cactcacaa caatcaatga taggccaaag 1020
caggcatggt gttggttttg aggaaaatgg aaggatgcaa taaaagaggt gaagcagacc 1080
attgtcaaac atcccaggta tactggaact aacaatactg ataaaatcaa tttgacggct 1140
cctggaggag gagatccgga agttaccttc atgtggacaa attgcagagg agagttcctc 1200
tactgtaaaa tgaattgggt tctaaattgg gtagaagata ggaatacagc taaccagaag 1260
ccaaaggaac agcataaaaag gaattacgtg ccatgtcata ttagacaaat aatcaacact 1320
tggcataaag taggcaaaaa tgtttatatt cctccaagag agggagacct cacgtgtaac 1380
tccacagtga ccagtctcat agcaaacata gattggattg atggaaacca aactaatatc 1440
accatgagtg cagaggtggc agaactgtat cgattggaat tgggagatta taaattagta 1500
gagatcactc caattggctt ggccccccaca gatgtgaaga ggtacactac tgggtggcacc 1560
tcaagaaata aaagaggggt ctttgtgcta gggttcttgg gttttctcgc aacggcaggt 1620
tctgcaatgg gagccggcag cctgaccctc acggcacagt cccgaacttt attggctggg 1680
atagtccaac agcagcaaca gctgttggac gtggtcaaga gacaacaaga attggtgcga 1740
ctgaccgtct ggggaacaaa gaacctccag actagggtca ctgccatcga gaagtactta 1800
aaggaccagg cgcagctgaa tgcttgggga tgtgcgttta gacaagtctg ccacactact 1860
gtaccatggc caaatgcaag tctaacacca aagtggaaca atgagacttg gcaagagtgg 1920
gagcgaaagg ttgacttctt ggaagaaaa ataacagccc tcctagagga ggcacaaatt 1980
caacaagaga agaacatgta tgaattacaa aagttgaata gctgggatgt gtttggcaat 2040
tggtttgacc ttgcttcttg gataaagtat atacaatatg gagtttatat agttgtagga 2100
gtaatactgt taagaatagt gatctatata gtacaaatgc tagctaagtt aaggcagggg 2160
tataggccag tgttctcttc cccaccctct tatttccagc agaccatat ccaacaggac 2220
ccggcactgc caaccagaga aggcaaagaa agagacggtg gagaaggcgg tggcaacagc 2280
tcttggcctt ggcagataga atatatccac tttcttattc gtcagcttat tagactcttg 2340
acttggctat tcagtaactg taggactttg ctatcgagag tataccagat cctccaacca 2400
atactccaga ggctctctgc gaccctacag aggattcgag aagtcctcag gactgaactg 2460
acctacctac aatatgggtg gagctatttc catgaggcgg tccaggccgt ctggagatct 2520
gcgacagaga ctcttgcggg cgcggtggga gacttatggg agactcttag gagaggtgga 2580
agatggatac tcgcaatccc caggaggatt agacaagggc ttgagctcac tctcttgtga 2640
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<210> 19

<211> 813

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: coding sequence of  
complementary strand positions 6426-5611 of vector  
CMVkan/R-R-SIVenvCTE (SEQ ID NO:15)

<400> 19

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gctgatttat atgggtataa atgggctcgc gataatgtcg ggcaatcagg tgcgacaatc 120
tatcgattgt atgggaagcc cgatgcgcca gagttgtttc tgaaacatgg caaaggtagc 180
gttgccaatg atgttacaga tgagatggtc agactaaact ggctgacgga atttatgcct 240
cttccgacca tcaagcattt tatccgtact cctgatgatg catggttact caccactgcg 300
atccccggga aaacagcatt ccaggatta gaagaatatc ctgattcagg tgaaaatatt 360
gttgatgcgc tggcagtgtt cctgcgccgg ttgcattcga ttcctgtttg taattgtcct 420
tttaacagcg atcgcgtatt tcgtctcgcg caggcgcaat cacgaatgaa taacggtttg 480
gttgatgcga gtgattttga tgacgagcgt aatggctggc ctgttgaaca agtctggaaa 540
gaaatgcata agctttttgcc attctcaccg gattcagtcg tcaactcatg tgatttctca 600
cttgataaacc ttatttttga cgaggggaaa ttaatagggt gtattgatgt tggacgagtc 660
ggaatcgcag accgatacca ggatcttgcc atcctatgga actgcctcgg tgagttttct 720
ccttcattac agaaacggct ttttcaaaaa tatggtattg ataatcctga tatgaataaa 780
ttgcagtttc atttgatgct cgatgagttt ttc 813
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<210> 20

<211> 1532

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus  
sequence of mutated SIVgagDX and wild type  
Simian (macaque) immunodeficiency virus  
isolate 239, clone lambda siv 239-1

<400> 20

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ctacgaccca acggaaagaa aaagtacatg ttgaagcatg tagtatgggc agcaaatgaa 120
ttagatagat ttggattagc agaaagcctg ttggagaaca aagaaggatg tcaaaaaata 180
ctttcgggtct tagctccatt agtgccaaca ggctcagaaa atttaaaaag cttttataat 240
actgtctgcg tcatctggtg cattcacgca gaagagaaaag tgaaacacac tgaggaagca 300
aaacagatag tgcagagaca cctagtgggtg gaaacaggaa cmacmgaaac yatgccraar 360
acmwstmgac caacagcacc atctagcggc agaggaggaa aytaccagat acarcaratm 420
ggtggttaact aygtccacct gccaytrwsc ccgagaacmy traaygcytg ggtmaarytg 480
atmgaggara agaarttygg agcagaagta gtgccaggat tycaggcact gtcagaaggt 540
tgcacccctc aygacatyaa ycagatgytr aaytgygtkg gagaccatca rgcggctatg 600
cagatyatcm gwgayatyat maacgaggag gctgcagatg ggacttgcag caccacaac 660
cagctccaca acaaggacaa cttaggggagc cgtcaggatc agayatygca ggaacmacyw 720
sytcagtwga ygaacaratc cagtggatgt acmgwcarca gaacccsatm ccagtaggca 780
acatytacmg kmgatggatc carctgggky tgcarartg ygtymgwatg tayaaccra 840
cmaacattct agatgtaaaa caagggccaa aagagccatt tcagagctat gtagacaggt 900
tctacaaaag tttaagagca gaacagacag atgcagcagt aaagaattgg atgactcaa 960
cactgctgat tcaaaatgct aaccagatt gcaagctagt gctgaagggg ctgggtgtga 1020
atcccaccct agaagaaatg ctgacggctt gtcaaggagt agggggggccg ggacagaagg 1080
ctagattaat ggcagaagcc ctgaaagagg ccctcgcacc agtgccaatc ccttttgcag 1140
cagcccaaca gaggggacca agaaagccaa ttaagtgttg gaattgtggg aaagaggac 1200
actctgcaag gcaatgcaga gccccaagaa gacagggatg ctggaaatgt ggaaaaatgg 1260
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gaaagaagcc ccgcaatttc cccatggctc aagtgcacat ggggctgatg ccaactgctc 1380
ccccagagga cccagctgtg gatctgctaa agaactacat gcagttgggc aagcagcaga 1440
gagaaaagca gagagaaagc agagagaagc cttacaagga ggtgacagag gatttgctgc 1500
acctcaattc tctcttttga ggagaccagt ag 1532
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